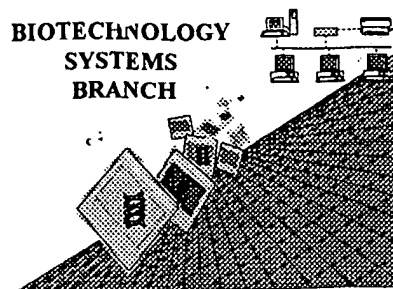


RAW SEQUENCE LISTING ERROR REPORT



1645
#4

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/671,687

Source: BATCH-RUSH

Date Processed by STIC: 3/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable Form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED
APR 20 2001
TECH CENTER 1600/2900

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/67/687

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

BATCH

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001

TIME: 09:34:53

Input Set : A:\Wallach.app

Output Set: N:\CRF3\03292001\I671687.raw

Does Not Comply
Corrected Diskette Needed

pg 1-2

3 <110> APPLICANT: WALLACH, David
 4 KOVALENKO, Andrei
 5 CANTARELLA, Giuseppina
 7 <120> TITLE OF INVENTION: Inhibitor of NF-kB Activator
 9 <130> FILE REFERENCE: WALLACH=25
 11 <140> CURRENT APPLICATION NUMBER: US/09/671,687
 12 <141> CURRENT FILING DATE: 2000-09-28
 14 <150> PRIOR APPLICATION NUMBER: PCT/IL99/00158
 15 <151> PRIOR FILING DATE: 1999-03-18
 17 <150> PRIOR APPLICATION NUMBER: 09/646,403
 18 <151> PRIOR FILING DATE: 2000-09-18
 20 <150> PRIOR APPLICATION NUMBER: IL 126024
 21 <151> PRIOR FILING DATE: 1998-09-01
 23 <150> PRIOR APPLICATION NUMBER: IL 134604
 24 <151> PRIOR FILING DATE: 2000-02-17
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 32 <212> TYPE: DNA
 33 <213> ORGANISM: HUMAN
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 38 ccaatggaag tattggccac agtccacttt ctctgtcagc ccagtctgta atggaagagc 180
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see item 10 on Encl
Summary Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001
TIME: 09:34:53

Input Set : A:\Wallach.app
Output Set: N:\CRF3\03292001\I671687.raw

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66 gcagttctgt tcacggtcca ttgcccggca tggatgtctt tgtggtgatg atccttcaga 1860
67 aaaggatgcc tctgtttaaa aacaaattgc ttttgtgtcc ctgaagtatt taataagaag 1920
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84 tcttcatgga aaattgataa atatttgtgc ctccaactc tcttcttggg tgaatgactt 360
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see item 10

item 10

item 10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001

TIME: 09:34:53

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Output Set: N:\CRF3\03292001\I671687.raw

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142 <210> SEQ ID NO: 3

143 <211> LENGTH: 949

144 <212> TYPE: PRT

145 <213> ORGANISM: HUMAN

147 <400> SEQUENCE: 3

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152 20 25 30
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155 35 40 45
157 Tyr Ile Gln Asp Arg Ser Val Gly His Ser Arg Ile Pro Ser Ala Lys
158 50 55 60
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161 65 70 75 80
163 Val Leu Phe Val Asp Glu Asp Val Val Glu Ile Asn Glu Lys Phe Thr
164 85 90 95
166 Glu Leu Leu Leu Ala Ile Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe
167 100 105 110
169 Lys Asn Arg Asn Arg Leu Ser Lys Gly Leu Gln Ile Asp Val Gly Cys

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001

TIME: 09:34:53

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Output Set: N:\CRF3\03292001\I671687.raw

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178 Phe Phe Gly Val Glu Leu Leu Glu Glu Gly Arg Gly Gln Gly Phe Thr
179          165          170          175
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182          180          185          190
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185          195          200          205
187 Ala Leu Glu Ser Asp Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu
188          210          215          220
190 Leu Pro Pro Leu Glu Ile Asn Ser Arg Val Ser Leu Lys Gly Gly Glu
191 225          230          235          240
193 Thr Ile Glu Ser Gly Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys
194          245          250          255
196 Glu Ser Leu Gly Tyr Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly
197          260          265          270
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200          275          280          285
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203          290          295          300
205 Thr Gln Glu Arg Arg Pro Pro Lys Leu Ala Phe Met Ser Arg Gly Val
206 305          310          315          320
208 Gly Asp Lys Gly Ser Ser Ser His Asn Lys Pro Lys Ala Thr Gly Ser
209          325          330          335
211 Thr Ser Asp Pro Gly Asn Arg Arg Ser Glu Leu Phe Tyr Thr Leu Asn
212          340          345          350
214 Gly Ser Ser Val Asp Ser Gln Pro Gln Ser Lys Ser Lys Asn Thr Trp
215          355          360          365
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218          370          375          380
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221 385          390          395          400
223 Asn Ser Leu Thr Thr Glu Asn Arg Phe His Ser Leu Pro Phe Ser Leu
224          405          410          415
226 Thr Lys Met Pro Asn Thr Asn Gly Ser Ile Gly His Ser Pro Leu Ser
227          420          425          430
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230          435          440          445
232 Glu Ser Pro Pro Leu Ala Met Pro Pro Gly Asn Ser His Gly Leu Glu
233          450          455          460
235 Val Gly Ser Leu Ala Glu Val Lys Glu Asn Pro Pro Phe Tyr Gly Val
236 465          470          475          480
238 Ile Arg Trp Ile Gly Gln Pro Pro Gly Leu Asn Glu Val Leu Ala Gly
239          485          490          495
241 Leu Glu Leu Glu Asp Glu Cys Ala Gly Cys Thr Asp Gly Thr Phe Arg
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001

TIME: 09:34:53

Input Set : A:\Wallach.app

Output Set: N:\CRF3\03292001\I671687.raw

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247 Leu Lys Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val
248          530          535          540
250 Ser Asn Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu
251 545          550          555          560
253 Ser Glu Val Val Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly
254          565          570          575
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266 625          630          635          640
268 Leu Arg Ile Tyr Gly Tyr Val Cys Ala Thr Lys Ile Met Lys Leu Arg
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271 Lys Ile Leu Glu Lys Val Glu Ala Ala Ser Gly Phe Thr Ser Glu Glu
272          660          665          670
274 Lys Asp Pro Glu Glu Phe Leu Asn Ile Leu Phe His His Ile Leu Arg
275          675          680          685
277 Val Glu Pro Leu Leu Lys Ile Arg Ser Ala Gly Gln Lys Val Gln Asp
278          690          695          700
280 Cys Tyr Phe Tyr Gln Ile Phe Met Glu Lys Asn Glu Lys Val Gly Val
281 705          710          715          720
283 Pro Thr Ile Gln Gln Leu Leu Glu Trp Ser Phe Ile Asn Ser Asn Leu
284          725          730          735
286 Lys Phe Ala Glu Ala Pro Ser Cys Leu Ile Ile Gln Met Pro Arg Phe
287          740          745          750
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296 785          790          795          800
298 Ile Ser Ala Gly Lys Ile Lys Gln Phe Cys Lys Thr Cys Asn Thr Gln
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308          850          855          860
310 Tyr Val Ala Phe Val Lys Tyr Gly Lys Asp Asp Ser Ala Trp Leu Phe
311 865          870          875          880
313 Phe Asp Ser Met Ala Asp Arg Asp Gly Gly Gln Asn Gly Phe Asn Ile
314          885          890          895
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001
TIME: 09:34:54

Input Set : A:\Wallach.app
Output Set: N:\CRF3\03292001\I671687.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:45 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:45 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:45 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:45 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:45 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:47 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:79 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:79 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:91 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:91 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:91 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:91 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:101 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2